

ANNOTATED FIG. 1

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.1 [Aug-1-2001]

Matrix: BLOSUM62 gap open: 11 gap extension: 1
 x_dropoff: 15 expect: 10.0 wordsize: 3 Filter: []

Sequence 1 |cl|seq_1 Length 510 (1..510)..

Sequence 2 |cl|seq_2 Length 512 (1..512)

2

NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

Score = 786 bits (2029), Expect = 0.0
 Identities = 419/522 (80%), Positives = 448/522 (85%), Gaps = 22/522 (4%)

Query: 1	MFIESFRVESPHVRYGAAEIESDYQYDTTEL VHESHGASRWIVRPKSVRYNERTTTTVP	SEQ ID 2
60	MFIESFRVESPHVRYGAAEIES+Y+YDTTEL VHESHGASRW+VREKSV+Y+ERT+TTVP	
Sbjct: 1	MFIESFRVESPHVRYGAAEIESEYRYDTTEL VHESHGASRWVVRPKSVQYHFTSTTTVP	SEQ ID 3
60		
Query: 61	KLGVMLVGWGGNNGSTLTAGVIANREGISWATKDKVQQANYGSLTQASTIRVGSYNGEE	SEQ ID 2
120	KLGVMLVGWGGNNGSTLTAGVIA+REGISWATKDKVQQANYGSLTQASTIRVGSYNGEE	
Sbjct: 61	KLGVMLVGWGGNNGSTLTAGVIASREGISWATKDKVQQANYGSLTQASTIRVGSYNGEE	SEQ ID 3
120		
Query: 121	IYAPFKSLLPMVNPDDLVEGGWDISNMNLADAMTRAKVLDIDLQQLRPYMES-----	SEQ ID 2
173	IYAPFKSLLPMVNPDDLVFEGGWDISNMNLADAMTRAKVLDIDLQQLRPYMES	
Sbjct: 121	IYAPFKSLLPMVNPDDLVEGGWDISNMNLADAMTRAKVLDIDLQQLRPYMESWCLSLAS	SEQ ID 3
180		
Query: 174	MVPL--PGIYDFDVIAANQGSRRANNVIKGTKEQMEQIIKDIREFKEKSKVDKVVVLTWA	SEQ ID 2
231	M+P . P DP A SR ++ + + KDIREFKE IK+DK VVLTWA	
Sbjct: 181	KIPTSSPLTRDF---ARTMSSRE-----PRRSRWGRSSKDIREFKENNKMDKAVVLTWA	SEQ ID 3
231		

Fig: 1

Query: 232 NTERYSN-VCVGLNDTMENLLASVDKNEAISPSTLYAIACV-MEGIPFIINGS PQNTFVP 289 SEQ ID 2
 NTERY+N ICIGL T ASVDINIAEISPSTLY IEG+ I G+ + P
 Sbjct: 232 NTERYNHCLCLGLM-TNGKPSASVDRNQAEISPSTLYCHCLASLEGVRSITGALKKSWP 290 SEQ ID 3

Query: 290 GLIDLAIKNNCLI-GGDDFKSGQTKMKSVLVDFLVGAGIKPTSIVSYNHLGNNDG NLSA 348 SEQ ID 2
 G+ DLAIK GG K G+ K K+ LVDFL+GAGIKPTSIVSYNHLGNNDG NLSA
 Sbjct: 291 GIDDLAIKKKLPDPGGLIQKRGKPKKKTGLVDFLMGAGIKPTSIVSYNHLGNNDG NLSA 350 SEQ ID 3

Query: 349 PQFRSKEISKSNVDDMVSSNAILYELGEHPDHVVVIKYVPYVGDSKRAMDEYTTSEIFM 408 SEQ ID 2
 PQFRSKEISKSNVDDMVSSNAILYELGEHPDHVVVIKYVPYVGDSKRAMDEYTTSEIFM
 Sbjct: 351 PQFRSKEISKSNVDDMVSSNAILYELGEHPDHVVVIKYVPYVGDSKRAMDEYTTSEIFM 410 SEQ ID 3

Query: 409 GKGSTIVLHNTCEDSLAAPIILDVLVLAELSTRIQLKAEGERKFHSEHPVATILSYLTK 468 SEQ ID 2
 GKG+TIVLHNTCEDSLAAPIILDVLVLAELSTRIQLKAEGERKFHSEHPVATILSYLTK
 Sbjct: 411 GKGNTIVLHNTCEDSLAAPIILDVLVLAELSTRIQLKAEGERKFHSEHPVATILSYLTK 470 SEQ ID 3

Query: 469 APLVPPGTFPVVNALAKQRAMLENIMRACVGLAPENNMILEYK 510. SEQ ID 2
 APLVPPGTFPVVNALAKQRAMLENIMRACVGLAPENNMILEYK
 Sbjct: 471 APLVPPGTFPVVNALAKQRAMLENIMRACVGLAPENNMILEYK 512 SEQ ID 3
 CPU time: 0.10 user secs. 0.02 sys. secs 0.12 total
 secs.

Gapped
 Lambda K H
 0.316 0.134 0.385

Gapped
 Lambda K H
 0.267 0.0410 0.140

Matrix: BLOSUM62
 Gap Penalties: Existence: 11, Extension: 1
 Number of Hits to DB: 2125
 Number of Sequences: 0
 Number of extensions: 153
 Number of successful extensions: 5
 Number of sequences better than 10.0: 1
 Number of HSP's better than 10.0 without gapping: 1
 Number of HSP's successfully gapped in prelim test: 0
 Number of HSP's that attempted gapping in prelim test: 0
 Number of HSP's gapped (non-prelim): 1
 length of query: 510
 length of database: 233,319,389
 effective HSP length: 125
 effective length of query: 385
 effective length of database: 176,133,389
 effective search space: 67811354765
 effective search space used: 67811354765

Fig: 1 (Cont'd)